



# Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

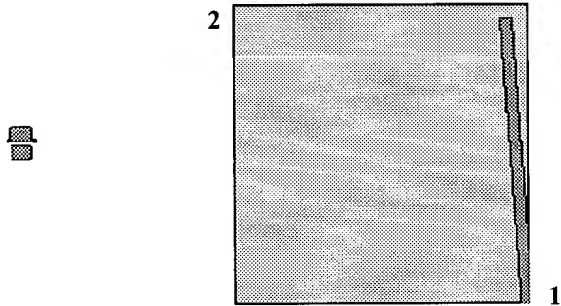
Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.3 [Apr-24-2002]

Match:  Mismatch:  gap open:  gap extension:   
 x\_dropoff:  expect:  wordsize:  Filter ☒ Align

**Sequence 1** [gi\\_4096271](#) Human MHC Class II HLA DRB1 gene, exon 2, partial cds. **Length** 262 (1 .. 262)

**Sequence 2** [lcl|seq\\_2](#) **Length** 19 (1 .. 19)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 37.2 bits (19), Expect = 8.3  
 Identities = 19/19 (100%)  
 Strand = Plus / Minus



Query: 244 gtgagagcttcacagtgc 262  
 |||||  
 Sbjct: 19 gtgagagcttcacagtgc 1

CPU time: 0.05 user secs. 0.05 sys. secs 0.10 total secs.

Lambda K H  
 1.33 0.621 1.12

Gapped  
 Lambda K H  
 1.33 0.621 1.12

Matrix: blastn matrix:1 -2  
 Gap Penalties: Existence: 5, Extension: 2  
 Number of Hits to DB: 1  
 Number of Sequences: 0  
 Number of extensions: 1  
 Number of successful extensions: 1  
 Number of sequences better than 10000.0: 1  
 length of query: 262  
 length of database: 5,692,721,829  
 effective HSP length: 24  
 effective length of query: 238

effective length of database: 5,564,683,269  
effective search space: 1324394618022  
effective search space used: 1324394618022  
T: 0  
A: 30  
X1: 6 (11.5 bits)  
X2: 26 (50.0 bits)  
S1: 12 (23.8 bits)  
S2: 14 (27.6 bits)